29.	Adamowicz, et al., "Nutritional complementation of oxidative glucose metabolism in Escherichia coli via pyrroloquinoline quinone-dependent glucose dehydrogenase and
Ma.	the Entner-Doudoroff pathway," Appl Environ Microbiol, 57(7):2012-2015 (1991).
30.	Alberty, "Calculation of Biochemical Net Reactions and Pathways by Using Matrix
30.	Operations," <u>Biophys J</u> , 71(1):507-515 (1996).
31.	Im, et al., "Genomic-sequence comparison of two unrelated isolates of the human
	gastric pathogen Helicobacter pylori," Nature, 397(6715):176-80 (1999). Alon et al., "Broad patterns of gene expression revealed by clustering analysis of umor
32.	and normal colon tissues probed by oligonucleotide arrays," Proc Natl Acad Sci U.S.A.,
	96(12):6745-6750 (1999).
33.	Alter, et al., "Singular value decomposition for genome-wide expression data
	processing and modeling," Proc Natl Acad Sci U.S.A., 97(18):10101-10106 (2000).
34.	Altschul, et al., Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs," Nucl Acids Res, 25(17):3389-3402 (1997).
	Alves, et al., "Systemic properties of ensembles of metabolic networks: application of
35.	graphical and statistical methods to simple unbranched pathways," Bioinformatics,
	16(6):534-547 (2000).
36.	Andre, "An overview of membrane transport proteins in Saccharomyces cerevisiae,"
37.	<u>Yeast</u> , 11(16):1575-1611 (1995). Anonymous, "The yeast genome directory" <u>Nature</u> , 38/(6632 Suppl):5 (1997).
	Appel, et al., "A new generation of information retrieval tools for biologists: the
38.	example of the ExPASy WWW server," <u>Trends Biochem Sci</u> , 19(6):258-260 (1994).
39.	Attanoos, et al., "Ileostomy polyps, adenomas, and adenocarcinomas," Gut, 37(6):840-
	844 (1995).
40.	Baba, et al., "Construction of Escherichia & i K-12 in-frame, single-gene knockout mutants: the Keio collection," Mol Syst Biol, 2:2006-2008 (2006).
14	Bailey, "Complex Biology With No Parameters," Nat Biotechnol, 19(6):503-504
41.	(2001).
42.	Bailey, TL and Elkan, C, "Fitting a mixture model by expectation maximization to
	discover motifs in biopolymers, Proc Int Conf Intell Syst Mol Biol, 2:28-36 (1994). Bailey, TL and Gribskov, M. Combining evidence using p-values: application to
43.	sequence homology searches," <u>Bioinformatics</u> , 14(1):48-54 (1998).
44	Bairoch, A, and Apweiler, R, "The SWISS-PROT Protein Sequence database and its
44.	supplement TrEMBL in 2000," Nucleic Acids Res, 28(1):45-48 (2000).
45.	Ball, et al., "Integrating functional genomic information into the Saccharomyces
-	genome database Nucleic Acids Res, 28(1):77-80 (2000). Ban, et al., "The mine and uracil catabolism in Escherichia coli," J Gen Microbiol,
46.	73(2):267-272 (1972).
47.	Bansal, "Integrating co-regulated gene-groups and pair-wise genome comparisons to
	automate reconstruction of microbial pathways," Bioinformatics and Bioengil eering
	Conference, 209-216 (2001). Bard, et al., "Sterol mutants of Saccharomyces cerevisiae: chromatographic analyses,"
48.	Lipids, 12(8):645-654 (1977).
49.	Baxevanis, "The Molecular Biology Database Collection: 2002 update," Nucleic Acid
49.	Res, 30:1-12 (2002).
8 0.	Beard, et al., "Energy Balance for Analysis of Complex Metabolic Networks,"
	Biophys J, 83(1):79-86 (2002).

51.	Beckers, et al., "Large-Scale Mutational Analysis for the Annotation of the Mouse Genome," Curr Opin Chem Biol, 6(1)17-23 (2002).
1	Bell, et al., "Composition and functional analysis of the Saccharomyces cerevisiae
\$2.	trehalose synthase complex," <u>J Biol Chem.</u> , 273(50):33311-33319 (1998).
53.	Benson, et al., "GenBank," Nucleic Acids Res, 28(1):15-18 (2000).
54.	Rerry, "Improving production of aromatic compounds in Escherichia coli by metaboli engineering," Trends Biotechnol, 14(7):250-256 (1996).
55.	Bial, "Living on the Edges," Nat Biotechnol, 19(2):111-112 (2001).
56.	Bianch, P, and Zanella, A, "Hematologically Important Mutations: Red Cell P ruvate Kinase (Nird Update)," Blood Cells, Molecules, and Diseases, 15:47-53 (2000).
57.	Biaudet, et al., "Micado – a network-oriented database for microbial genories," Comput Appl Biosci, \$3(4):431-438 (1997).
58.	Birkholz, "Fumaçate reductase of Helicobacter pylorian immunogenic protein," <u>J Med Microbiol</u> , 41(1):55-62 (1994).
59.	Birner, et al., "Roles of phosphatidylethanolamine and of its several biosynthetic pathways in Saccharon yees cerevisiae," Mol Biol Cell, 12(4):997-1007 (2001).
60.	Blackstock, WP and Weik MP, "Proteomics: quantitative and physical mapping of cellular proteins," Trends Diotechnol, 17(3):121-127 (1999).
61.	BMES/EMBS Conference, Proceedings of the First Joint, Vol. 2, p. 1217 (1999).
62.	Bochner, "New technologies to assess genotype-phenotype relationships," <u>Nat Rev Genet</u> , 4(4):309-314 (2003).
63.	Boles, E, et al., "Identification and characterization of MAE 1, the <i>Saccharomyces cerevisiae</i> structural gene encoding mitochondral malic enzyme," <u>J Bacteriol.</u> , 180(11):2875-2882 (1998).
64.	Boles, et al., "A family of hexosephosphate mutases in <i>Saccharomyces cerevisia</i> ," Eur J Biochem, 220(1):83-96 (1994).
65.	Boles, et al., "Characterization of a Jucose-repressed pyruvate kinase (Pyk2p) in Saccharomyces cerevisiae that is atalytically insensitive to fructose-1,6-bisphosphate," J Bacteriol, 179(9):2987-2993 (1997).
66.	Bonarius, et al., "Metabolic fux analysis of hybridoma cells in different culture media using mass balances," Biotechnol Bioeng, 50(3):299-318 (1996).
67.	Bono, et al., "Reconstruction of amino acid biosynthesis pathways from the complete genome sequence," Genome Research, 8(3):203-210 (1998).
68.	Bottomley, et al., "Cloning, sequencing, expression, purification and preliminary characterization of a type II dehydroquinase from Helicobacter pylor," <u>Biochem. J</u> , 319(Pt 2):559-565 (1996).
69.	Bourot, S and Karst, F, "Isolation and characterization of the Saccharomy es cerevisiae SUT1 gene involved in sterol uptake," Gene, 165(1):97-102 (1995).
70.	Burgard AP and Maranas, CD, "Probing the Performance Limits of the Eschetichia coli Metabolic Network Subject to Gene Additions or Deletions," <u>Biotechnol Brieng</u> , 74(5):364-375 (2001).
71.	Bargard, AP and Maranas, CD, "Review of the Enzymes and Metabolic Pathways (EMP) Database," Metab Eng, 3(3):193-194(2) (2001).
7/2.	Burgard, et al., "Minimal reaction sets for Escherichia coli metabolism under different growth requirements and uptake environments," <u>Biotechnol Prog</u> , 17(5):791-797 (2001).
7	

73.	Burgard, et al., "Optknock: a bilevel programming framework for identifying gene knockout strategies for microbial strain optimization," <u>Biotechnol Bioeng</u> , 84(6):647-657 (2003).
74	Burns, "Acetyl-CoA carboxylase activity in Helicobacter pylori and the requirement of increased CO2 for growth," Microbiology, 141(Pt 12):3113-3118 (1995).
75.	
76.	
77.	Chalver, et al., "Systematic identification of selective essential genes in Helicobayer pylori by genome prioritization and allelic replacement mutagenesis," <u>J Bacteriol</u> , 183(4):1259-1268 (2001).
78.	Chen, et al., "Characterization of the respiratory chain of Helicobacter pyloti," <u>FEMS</u> <u>Immunol Med Microbiol</u> , 24(2):169-174 (1999).
79.	Cherry, et al., "SGD: Saccharomyces Genome Database," <u>Nucleic Acids Res</u> , 26(1):73-79 (1998).
80.	
81.	Ciriacy, M and Breitenbach, I, "Physiological effects of seven different blocks in glycolysis in Saccharomy es cerevisiae," <u>J Bacteriol</u> , 139(1): 52-160 (1979).
82.	Clarke, "Complete set of steady states for the general stoic hometric dynamical system," <u>J Chem Phys</u> , 75(10) 4970-4979 (1981).
83.	Clarke, "Stoichiometric network analysis," Cell Biophys, 12:237-253 (1988).
84.	
85.	Clifton, D and Fraenkel, DG, "Mutant studies of yeast phosphofructokinase.," <u>Biochemistry</u> , 21(8):1935-1942 (1982).
86.	Clifton, et al., "Glycolysis mutants in Saccharomyces cerevisiae.," Genetics, 88(1):1-11 (1978).
87.	Compan, I and Touati, D, et al., "Anaerobic activation of arcA transcription in Escherichia coli: roles of Fnr and Arc," Mol Microbiol, 11(5):955-964 (1994).
88.	Costanzo, et al., "YPD, PombePD and WormPD: model organism volumes of the BioKnowledge library, an integrated resource for protein information," <u>Nucleic Acids</u> Res, 29(1):75-9 (2001).
89.	Cotter, et al., "Aerobic regulation of cytochrome d oxidas (cydAB) operon expression in Escherichia coli: roles of Fnr and ArcA in repression and activation," Mol Microbiol, 25(3):605-615 (1997).
90.	
91.	Covert, et al., "Metabolic Modeling of Microbial Strains <i>In Silico</i> , Trends Biochem Sci, 26(3):179-186 (2001).
92.	Covert, et al., "Kegulation of Gene Expression in Flux Balance Models of Metabolism," J Theor Biol. 213(1):73-88 (2001).
93.	Covert, MW and Palsson, BO, "Constraints-based models: Regulation of Gone Expression Reduces the Steady-state Solution Space," J Theor Biol, 216 (2003)
94.	Covery, MW and Palsson, BO, "Transcriptional Regulation in Constraints-based Metholic Models of Escherichia coli," J Biol Chem, 277(31):28058-28064 (2002)
95.	Capp, JR and McAlister-Henn, L, "Cloning and Characterization of the gene encoding the IDH1 subunit of NAD(+)-dependent isocitrate dehydrogenase from <i>Saccharomyces cerevisiae</i> ," J Biol Chem, 267(23):16417-16423 (1992).
6.	D'Haeseleer, et al., "Genetic network inference: from co-expression clustering to reverse engineering," <u>Bioinformatics</u> , 16(8):707-726 (2000).

	Danchin, "Comparison Between the Escherichia coli and Bacillus subtilis Genomes
97.	Suggests That a Major Function of Polynucleotide Phosphorylase is to Synthesize
N. S.	CDP," <u>DNA Research</u> , 4(1):9-18 (1997).
	Dandekar, et al., "Pathway Alignment: Application to the Comparative Analysis of
98	Glycolytic Enzymes," <u>Biochem J</u> , 343(Pt 1):115-124 (1999).
	Qantigny, et al., "A new control strategy for yeast production based on the L/A*
99.	approach," Appl Microbiol Biotechnol, 36:352-357 (1991).
	Datsenko, KA and Wanner, BL, "One-step inactivation of chromosomal genes in
400	
100.	Escherichia coli K-12 using PCR products," Proc Natl Acad Sci U.S.A., 97(12):6640-
	6645 (2000).
101.	Daum, et al. "Biochemistry, cell biology and molecular biology of lipids of
	Saccharomyces cerevisiae," <u>Yeast</u> , 14(16):1471-1510 (1998).
102.	Daum, et al., "Systematic analysis of yeast strains with possible defects in lipid
	metabolism," Yeart, 15(7):601-614 (1999).
103.	Dauner, et al., "Backlus subtilis Metabolism and Energetics in Carbon-Limited and
100.	Excess-Carbon Chemostat Culture," J Bacteriol, 183(24):7308/7317 (2001).
104.	Dauner, et al., "Metabolic Flux Analysis with a Comprehensive Isotopomer Model in
104.	Bacillus subtilis," Biotechnol Bioeng, 76(2):144-156 (2007).
105.	Dauner, M and Sauer, U, "Staichiometric Growth Model for Riboflavin-Producing
105.	Bacillus subtilis," Biotechnol Bioeng, 76(1):132-143 (2001).
100	de Jong, H., "Modeling and simulation of genetic regulatory systems: a literature
106.	review," J Comput Biol, 9(1):67-103 (2002).
	De Reuse, et al., "The Helicobacter pyori ureQ gene codes for a phosphoglucosamine
107.	mutase," J Bacteriol, 179(11):3488-3493 (1997).
	Delgado and Liao, "Identifying Rate-Contylling Enzymes in Metabolic Pathways
108.	without Kinetic Parameters," <u>Biotechnol Pros.</u> 7:15-20 (1991).
-	Demain, et al., "Cellulase, clostridia, and ethanol," <u>Microbiol Mol Biol Rev</u> , 69(1):124-
109.	154 (2005).
110.	Department of Energy, Breaking the Biological Barkers to Cellulosic Ethanol (2006).
110.	DeRisi, et al., "Exploring the Metabolic and Genetic Control of Gene Expression on a
111.	Conomic Scale "Science 27/(5229).(90, 696 (1907)
	Genomic Scale," Science, 278(5338):680-686 (1997).
112.	Devine, KM, "The Bacillus subtilis Genome Project: Aims and Progress," Trends
	Biotechnol, 13(6):210-2/6 (1995). Dickson, "Sphingolipid Functions in Sacchoromyces Cerevisiae: Comparison to
113.	Dickson, "Sphingolipid Functions in Sacchoromyces Cerevisiae: Comparison to
	Mammals," Annu Rev Biochem, 67:27-48 (1998).
114.	Dickson, et al., "Serine palmitoyltransferase," Methods Enzymol, 3 N:3-9 (2000).
	DiRusso, CC and Black, PN, "Long-chain fatty acid transport in bacteria and yeast.
115.	Paradigms for defining the mechanism underlying this protein-mediated process," Mol
	<u>Cell Biochem</u> , 192(1-2):41-52 (1999).
116.	
117.	Edwards, et al., "Characterizing the Metabolic Phenotype: A Phenotype Phase Nane
117.	Analysis," <u>Biotech Bioeng</u> , 77(1):27-36 (2002).
140	Edwards, et al., "In Silico Predictions of Escherichia coli metabolic capabilities are
118.	Consistent with Experimental Data," Nat Biotechnol, 19(2):125-130 (2001).
	Edwards, JS and Palsson, BO, "Robustness analysis of the Escherichia coli metabolic
11/9.	network," <u>Biotechnol Prog</u> , 16(6):927-939 (2000).

120.	Edwards, JS, and Palsson, BO, "Metabolic flux balance analysis and the <i>in silico</i> analysis of Escherichia colia K-12 gene deletions," <u>BMC Bioinformatics</u> , 1:1-10 (2000).
124.	Eisen, et al., "Cluster analysis and display of genome-wide expression patterns," <u>Proc Natl Acad Sci U.S.A.</u> , 95:14863-14868 (1998).
122.	Fisenberg, et al., "Protein Function in the Post-Genomic Era," Nature, 405(6788):823/826 (2000).
123.	Ermelaeva, et al., "Prediction of Operons in Microbial Genomes," Nucl Acids Research, 29(5):1216-1221 (2001).
124.	
125.	Fiehn, "Menbolomicsthe link between genotypes and phenotypes," Plan Mol Biol, 48(1-2):155-121 (2002).
126.	Finel, "Does NADH play a central role in energy metabolism in Helicobacter pylori?," Trends Biochem Sci, 23(11):412-413 (1998).
127.	Fiorelli, et al., "Chronic non-spherocytic haemolytic disorders associated with glucose-6-phosphate dehydrogenase variants," <u>Bailliere's Clinical Haematology</u> , 13:39-55 (2000).
128.	
129.	Flikweert, et al., "Pyruvate decarboxylase: an indispensable enzyme for growth of Saccharomyces cerevisiae on glycose.," Yeast, 12(3):247-257 (1996).
130.	Forst, "Network genomics A Novel approach for the analysis of biological systems in the post-genomic era," Molecular Biology Reports, 29(3):265-280 (2002).
131.	Forster, et al., "Large-scale evaluation of in silico gene deletions in Saccharomyces cerevisiae," Omics, 7(2)193-202 (2003).
132.	Fraenkel, "The accumulation of glucose 6-phosphate from glucose and its effect in an Escherichia coli mutant lacking phosphoglucose isomerase and glucose 6-phosphate dehydrogenase," J Biol Chem, 243(24):6451-6457 (1968).
133.	Fraser, et al., "Microbial genome sequencing," Nature, 406:799-803 (2000).
134.	Fromont-Racine, et al., "Toward functional analysis of the yeast genome through exhaustive two-hybrid screens," Nat Genet, 16(3):277-282 (1997).
135.	Fukuchi, et al., "Isolation, overexpression and disruption of a Saccharomyces cerevisiae YNK gene encoding nucleoside diphosphate kinase," Gene. 129(1):141-146 (1993).
136.	Gaasterland, T. and Selkov, E., "Reconstruction of Metabolic Networks Using Incomplete Information," Proc Int Conf Intell Syst Mol Biol, 3: 27-135 (1995).
137.	Gancedo, C and Delgado, MA, "Isolation and characterization of a mutant from Saccharomyces corevisiae lacking fructose 1,6-bisphosphatase," <u>Eur J Biochem</u> , 139:651-655 (1984).
138.	Gangloff, et al., "Molecular cloning of the yeast mitochondrial aconitase tene (ACO1) and evidence of a synergistic regulation of expression by glucose plus glutamate.," Mol Cell Biol 10(7):3551-3561 (1990).
139.	
140.	Glasher, et al., "ASAP, a systematic annotation package for community analysis of genomes," Nucleic Acids Res, 31(1):147-151 (2003).
141	Goffeau, A, "Four years of post-genomic life with 6000 yeast genes," FEBS Lett, 480(1):37-41 (2000).
142.	Goryanin, et al., "Mathematical simulation and analysis of cellular metabolism and regulation," <u>Bioinformatics</u> , 15(9):749-758 (1999).
A CONTRACTOR OF THE PARTY OF TH	

	143.	Goto, et al., "LIGAND database for enzymes, compounds and reactions," <u>Nucleic Acids Res</u> , 27(1):377-379 (1999).
	44.	Goto, et al., "LIGAND: chemical database for enzyme reactions," <u>Bioinformatics</u> , 14(7):591-599 (1998).
	145.	Grewal, et al., "Computer Modelling of the Interaction Between Human Choriogonadotropin and Its Receptor," Protein Engineering, 7(2):205-211 (1994).
	146.	Griffin, et al., "Complementary profiling of gene expression at the transcriptome and proteome levels in Saccharomyces cerevisiae," Mol Cell Proteomics, 1:323-333 (2002).
	147.	Grundy et al., "Regulation of the Bacillus subtilis acetate kinase gene by CcpA" J Bacterio, 175(22):7348-7355 (1993).
	148.	Guelzim, et al., "Topological and causal structure of the yeast transcriptional regulatory network," Nat Genet, 31(1):60-63 (2002).
	149.	Guetsova, et al., "The isolation and characterization of Saccharomyces cerevisiae mutants that constitutively express purine biosynthetic genes," Genetics, 147(2):383-397 (1997).
	150.	
	151.	Hardison, et al., "Globin Gene Server: A Prototype E-Mail Database Server Featuring Extensive Multiple Alignments and Data Compilation for Electronic Genetic Analysis," Genomics, 21(2):344-353 (1984).
	152.	Hartig, et al., "Differentially regulated malate synthase genes participate in carbon and nitrogen metabolism of S. cerevisiae.," <u>Nucleic Acids Res</u> , 20(21):5677-5686 (1992).
	153.	Hasty, et al., "Computational Studies of Gene Regulatory Networks: <i>In Numero</i> Molecular Biology," Nat Rev Genet, 2(4):268-2/9 (2001).
	154.	Hata, et al., "Characterization of a Saccharonyces cerevisiae mutant, N22, defective in ergosterol synthesis and preparation of [28, 4C]ergosta-5,7-dien-3 beta-ol with the mutant," J Biochem, 94(2):501-510 (1987).
	155.	Hatzimanikatis, et al., "Analysis and Design of Metabolic Reaction Networks Via Mixed-Interger linear Optimization," AIChE Journal, 42(5):1277-1292 (1996).
	156.	Hazell, et al., "How Helicobacter pylori works: an overview of the metabolism of Helicobacter pylori," Helicobacter, 2(1):1-12 (1997).
	157.	Heijnen, et al., "Application of balancing methods in modeling the penicillin fermentation," Biotechnology & Bioeng., 21:2175-2201 (1979).
	158.	Heinisch, et al., "Investigation of two yeast genes encoding putative isoenzymes of phosphoglycerate mutate.," Yeast, 14(3):203-213 (1998).
	159.	Heinrich, et al., "Metabolic regulation and mathematical models," <u>Prog Biophys Mol Biol</u> , 32(1):1-82 (1977).
	160.	Heinrich, et al., Stoichiometric Analysis," <u>The Regulation of Cellular Systems</u> , xix:75-111 and 372, hapman & Hall, New York (1996).
	161.	Henriksen, et al., "Growth energetics and metabolism fluxes in continuous cultures of Penicillium chrysogenum," J of Biotechnol, 45(2):149-164 (1996).
	162.	Heyer et al., "Exploring expression data: identification and analysis of coexpressed genes," Genome Res, 9(11):1106-1115 (1999).
	163.	Holter, et al., "Dynamic modeling of gene expression data," Proc Natl Acad Sci U.S. 1, 8(4):1693-1698 (2001).
	164.	Holter, et al., "Fundamental patterns underlying gene expression profiles: simplicity from complexity," <u>Proc Natl Acad Sci U.S.A.</u> , 97:8409-9414 (2000).
A STATE OF THE STA	165.	Houghten, "Generation and use of synthetic peptide combinatorial libraries for basic research and drug discovery," Nature, 354(6348):84-86 (1991).

166.	Hughes, et al., "Functional discovery via a compendium of expression profiles," <u>Cell</u> , 102(1):109-126 (2000).
107.	Hughes, et al., "Helicobacter pylori porCDAB and oorDABC genes encode distinct pyruvate: flavodoxin and 2-oxoglutarate:acceptor oxidoreductases which mediate electron transport to NADP," <u>J Bacteriol</u> , 180(5):1119-1128 (1998).
168.	Neker, et al., "Integrated Genomic and Proteomic Analyses of a Systematically Perurbed Metabolic Network," <u>Science</u> , 292(5518):929-934 (2001).
169.	Ince, E and Knowles, CJ, "Ethylene formation by cell-free extracts of Escherichic coli," Arch Microbiol, 146(2):151-158 (1986).
170.	Ishii, et al. "DBTBS: a database of Bacillus subtilis promoters and transcription factors," Nucleic Acids Res, 29(1):278-280 (2001).
171.	Iyer, et al., "Genomic binding sites of the yeast cell-cycle transcription factors SBF and MBF," Nature, 409(6819):533-538 (2001).
172.	Jamshidi, et al., "Dynamic simulation of the human red blood cell metabolic network," Bioinformatics, 17(3) 286-287 (2001).
173.	Jamshidi, et al., "In silico model-driven assessment of the effect of single nucleotide polymorphins (SNPs) on ruman red blood cell-metabolism," renome Research, 12(11):1687-1692 (2002).
174.	Jenkins, LS and Nunn, WD, "Cenetic and molecular characterization of the genes involved in short-chain fatty acid degradation in Escherichia coli: the ato system," <u>J Bacteriol</u> , 169(1):42-52 (1987).
175.	Jenssen, et al., "A Literature Network of Human Genes for High-Throughput Analysis of Gene Expression," Nat Genet, 28(1):21-28 (2001).
176.	Jorgensen, et al., "Metabolic flux distributions in <i>Penicillium chrysogenum</i> during fedbatch cultivations." <u>Biotechnol Bioeng</u> , 46(2):117-131 (1995).
177.	Joshi, A and Palsson, BO, "Metabolic dynamics in the human red cell. Part IA comprehensive kinetic model," <u>J Theor Biol</u> , 14 (4):515-528 (1989).
178.	Juty, et al., "Simultaneous Modeling of Metabolic, Genetic, and Product-Interaction Networks," <u>Briefings in Bioinformatics</u> , 2(3):223-232 (2001).
179.	Kanehisa, M and Goto, S, "Kyoto Encyclopedia of Genes and Genomes database (KEGG)," Nucleic Acids Res. 28(1):27-30 (2000).
180.	Karp, "An ontology for biological function based on molecular interactions," Bioinformatics, 16(3):269-285 (2000).
181.	Karp, et al., "Eco Cyc; encyclopedia of Escherichia coli genes and metabolism," Nucleic Acids Res, 2/(1):55-58 (1999).
182.	Karp, et al., "HinCyc: A knowledge base of the complete genome and metabolic pathways of H. influenzae," Proc Int Conf Intell Syst Mol Biol, 4:116-124 (1996).
183.	Karp, et al., "Integrated pathway-genome databases and their role in drug discovery.," Trends Biotechnol, 17(7):275-281 (1999).
184.	Karp, et al., "The EcoCyc and MetaCyc databases," <u>Nucleic Acids Resarch</u> , 28(1):56-59 (2000).
185.	Kather, et al., "Another unusual type of citric acid cycle enzyme in Helicobacter pylori: the malate:quinone oxidoreductase," J Bacteriol, 182(11):3204-3209 (2000).
186	Keating, et al., "An ethanologenic yeast exhibiting unusual metabolism in the fermentation of lignocellulosic hexose sugars," <u>J Ind Microbiol Biotechnol</u> , 31(5):235-244 (2004).
187.	
7	

188.	Kim, et al., "Saccharomyces cerevisiae contains two functional citrate synthase genes.," Mol Cell Biol, 6(6):1936-1942 (1986).
189.	Kirkman, et al., "Red cell NADP+ and NADPH in glucose-6-phosphate dehydrogenase deficiency," <u>Journal of Clinical Investigation</u> , 55(4):875-878 (1975).
190.	Kremling, et al., "The organization of metabolic reaction networks. III. Application for ajauxic growth on glucose and lactose," Metab Eng, 3(4):362-379 (2001).
191.	Kunst, et al., "The Complete Genome Sequence of the Gram-positive Bacterium Bacillus," Nature, 390(6557):249-256 (1997).
192.	Lacroute, "Regulation of pyrimidine biosynthesis in Saccharomyces cerevisiae" J Bacteriol, 95(3):824-832 (1968).
193.	Latif, F and Rajoka, MI, "Production of ethanol and xylitol from corn coby by yeasts," Bioresour Technol, 77(1):57-63 (2001).
194.	Lendenmann, U and Egli, T, "Is Escherichia coli growing in glucose-limited chemostat culture able to utilize other sugars without lag?," Microbiology, 141/Pt 1):71-78 (1995).
195.	Leyva-Vasquez, MA and Setlow, P, "Cloning and nucleotide sequences of the genes encoding triose phosphate isomerase, phosphoglycerate mutase, and enclase from Bacillus subtilis," J Bacteriol, 176(13):3903-3910 (1994).
196.	Li, C and Wong, WH, "Model-based analysis of oligonucl otide arrays: expression index computation and outlier detection," <u>Proc Natl Acad Sci U.S.A.</u> , 98(1):31-36 (2001).
197.	Liao, et al., "Pathway Analysis, Engineering, and Physiological Considerations for Redirecting Central Metabolism," Biotechnol Bioeng, 52(1):129-140 (1996).
198.	Liao, JC and Oh, MK, "Toward predicting metabolic fluxes in metabolically engineered strains," Metab Eng. 1(3):214-223 (1999).
199.	Link, et al., "Methods for generating precise deletions and insertions in the genome of wild-type <i>Escherichia coli</i> : Application to open reading frame characterization," J Bacteriol, 179(20):6228-6237 (1997).
200.	Loftus, et al., "Isolation, characterization, and disreption of the yeast gene encoding cytosolic NADP-specific isocitrate dehydrogenase," <u>Siochemistry</u> , 33(32):9661-9667 (1994).
201.	Lopez, et al., "The yeast inos fol monophosphatase is a libium- and sodium-sensitive enzyme encoded by a non-ssential gene pair," Mol Microbiol, 31(4):1255-1264 (1999).
202.	
203.	Maier, et al., "Hydrogen uptake hydrogenase in Helicobacter pylor" FEMS Microbiol Lett, 141(1):71-76 (1996).
204.	Marcelli, et al., The respiratory chain of Helicobacter pylori: identification of cytochromes and the effects of oxygen on cytochrome and menaquinone evels," <u>FEMS Microbiol Lett</u> , 138(1):59-64 (1996).
205.	
206.	McAdams, HH and Arkin, A, "Simulation of Prokaryotic Genetic Circuits," Annual Review of Biophysics and Biomolecular Structure, 27:199-224 (1998).
207.	
208	McAlister-Henn, L and Thompson, LM, "Isolation and expression of the gene encoding yeast mitochondrial malate dehydrogenase.," <u>J Bacteriol</u> , 169(11):5157-5166 (1987).
209.	McGee, D.J., "Helicobacter pylori rocF is required for arginase activity and acid protection in vitro but is not essential for colonization of mice or for urease activity," <u>J Bacteriol</u> , 165(1):65-76 (1998).

Res. 10(8):1081-1092 (2000). Mendes, P and Kell, D, "Non-linear optimization of biochemical pathways: Applications to metabolic engineering and parameter estimation," Bioinformatics, 14(10):869-883 (1998). 212. Mendz, et al., "Characterisation of glucose transport in Helicobacter pylori," Biochim Biophys Acta, 1244(2-3):269-276 (1995). 213. Mendz, et al., "Characterization of fumarate transport in Helicobacter pylori," J.M.m. Biol., 10s(1):65-76 (1998). 214. Mendz, et al., "De novo synthesis of pyrimidine nucleotides by Helicobacter pylori," Appl Bacteriol, 77(1):1-8 (1994). 215. 216. 217. Mendz, et al., "The stu characterization of Helicobacter pylori arginase," Biochim Biophys Acta, 1388(3):465-477 (1998). 218. Mendz, et al., "The Enther-Deudoroff pathway in Helicobacter pylori," Arch Biochem Microbiol, 168(6):448-458 (1997). 219. Mendz, et al., "The Enther-Deudoroff pathway in Helicobacter pylori," Arch Biochem Biophys, 312(2):349-356 (1994). 220. Mendz, GL and Hazell SL, "Amhoacid utilization by Flelicobacter pylori," Int J Biochem Cell Biol, 27(10):1085-1093 (1995). 221. Mendz, GL, et al., "Pyruvate metabolism in Helicobacter pylori," Arch Microbiol, 162(3):187-192 (1994). 222. Mendz, GL, et al., "Pyruvate metabolism in Helicobacter pylori," Arch Microbiol, 162(3):187-192 (1994). 223. Mendz, GL, et al., "Pyruvate metabolism in Helicobacter pylori," Arch Microbiol, 162(3):187-192 (1994). 224. Mewes, et al., "MIPS: A database for genomes and protein sequences," Nucleic Acid Research, 30(1):31-34 (2002). Mitchell, "The GLN1 locus of Saccharomyces cerevisia encodes glutamine synthetase," Genetics, 111(2):243-258 (1985). 226. Moszer, "The Complete Genome of Bacillus Subtilis: From Sequence Annotation to Data Management and Analysis," FEBS Lett, 430(1-2):28-36 (1998). 227. Mata Management and Analysis," EBS Lett, 430(1-2):28-36 (1998). 228. Moszer, et al., "Subtilist: the reference database for the bacillus subtilis genome," Nucleic Acids Res. 50(1):62-65 (2002). 229. Mulquiney, PJ apd Kuchel,		
Applications to metabolic engineering and parameter estimation," Bioinformatics. 14(10):869-833 (1998). 212. Mendz, et al., "Characterisation of glucose transport in Helicobacter pylori," Biochim Biophys Acta, 1244(2-3):269-276 (1995). 213. Mendz, et al., "Characterization of fumarate transport in Helicobacter pylori," J Mem Biol, 10s(1):65-76 (1998). 214. Mendz, et al., "De novo synthesis of pyrimidine nucleotides by Helicobacter pylori," Appl Bacteriol, 77(1):1-8 (1994). 215. 216. 217. Mendz, et al., "In stu characterization of Helicobacter pylori arginase," Biochim Biophys Acta, 1388(2):465-477 (1998). 218. Mendz, et al., "Purine metabolism and the microaerophily of Helicobacter pylori," A Microbiol, 168(6):448-458 (1997). 219. Mendz, et al., "Purine metabolism and the microaerophily of Helicobacter pylori," Arch Biochem Biophys, 312(2):349-356 (1994). 220. Mendz, et al., "The Entner-Doudoroff pathway in Helicobacter pylori," Arch Biochem Cell Biol, 27(10):1085-1093 (1995). 221. 222. Mendz, GL, and Hazell, SL, "Glucose phosphoroflation in Helicobacter pylori," Arch Biochem Biophys, 300(1):522-525 (1993). 223. Mendz, GL, et al., "Pyruvate metabolism in Helicobacter pylori," Arch Microbiol, 162(3):187-192 (1994). 224. 225. Mewes, et al., "MIPS: A database for genomes and protein sequences," Nucleic Acid Research, 30(1):31-34 (2002). 226. Mitchell, "The GLN1 locus of Saccharomyces cerevisiae encodes glutamine synthetase," Genetics, 111(2):7243-258 (1985). 227. Moszer, "The Complete Genome of Bacillus Subtilis: From Sequence Annotation to Data Management and Analysis," FEBS Lett, 430(1-2):28-36 (1998). 228. Moszer, et al., "Subtilist: the reference database for the bacillus subtilis genome," Nucleic Acids Res, 50(1):62-65 (2002). 229. Mulquiney, PJ and Kuchel, PW, "Model of 2,3-bisphosphoglycerate netabolism in thuman erythroy te based on detailed enzyme kinetic equations: computer simulation and metabolic control analysis," FEBS Lett, 430(1-2):28-36 (1999). 230. Moszer, et al., "Subtilist: th	210.	Meldrum, "Automation for genomics, part one: preparation for sequencing," Genome Res, 10(8):1081-1092 (2000).
 212. Biophys Acta, 1244(2-3):269-276 (1995). 213. Mende, et al., "Characterization of fumarate transport in Helicobacter pylori," J.M.m. Biol., 105(1):65-76 (1998). 214. Mende, et al., "De novo synthesis of pyrimidine nucleotides by Helicobacter pylori," Appl Bacteriol, 77(1):1-8 (1994). 215. 216. 217. Mendz, et al., "In situ characterization of Helicobacter pylori arginase," Biochim Biophys Acta, 1388 (3):465-477 (1998). 218. Mendz, et al., "Purine metabolism and the microaerophily of Helicobacter pylori," A Microbiol, 168(6):448-45x (1997). 219. Mendz, et al., "The Entner-Doudoroff pathway in Helicobacter pylori," Arch Biocher Biophys, 312(2):349-356 (1994). 220. Mendz, GL and Hazell SL, "Amnoacid utilization by Helicobacter pylori," Int J Biochem Cell Biol, 27(10):1085-1093 (1995). 221. Mendz, GL and Hazell, SL, "Glucose phosphory lation in Helicobacter pylori," Arch Biochem Biophys, 300(1):522-525 (1993). 222. Mendz, GL, et al., "Pyruvate metabolism in Helicobacter pylori," Arch Microbiol, 162(3):187-192 (1994). 223. Mewes, et al., "MIPS: A database for genomes and protein sequences," Nucleic Acid Research, 30(1):31-34 (2002). 226. Mitchell, "The GLN1 locus of Saccharomyces cerevisiae encodes glutamine synthetase," Genetics, 111(2):243-258 (1985). 227. Moszer, "The Complete Genome of Bacillus Subtilis: From sequence Annotation to Data Management and Analysis," FEBS Lett, 430(1-2):28-36 (1998). 228. Moszer, et al., "Subtilist: the reference database for the bacillus subtilis genome," Nucleic Acids Res. 50(1):62-65 (2002). 228. Mulquiney, P1 apd Kuchel, PW, "Model of 2,3-bisphosphoglycerate netabolism in the human erythroy/te based on detailed enzyme kinetic equations: compute simulation and metabolic control analysis," Biochem J, 342(Pt 3):597-604 (1999). 229. Murray, M and Greenberg, ML, "Expression of yeast INM1 encoding inositol monophysphatase is regulat	211.	Applications to metabolic engineering and parameter estimation," <u>Bioinformatics</u> , 14(10):869-883 (1998).
213. Biol. 165(1):65-76 (1998). 214. Mendz, et al., "De novo synthesis of pyrimidine nucleotides by Helicobacter pylori," Appl Bacteriol, 77(1):1-8 (1994). 215. 216. 217. Mendz, et al., "In stu characterization of Helicobacter pylori arginase," Biochim Biophys Acta, 1388(2):465-477 (1998). 218. Mendz, et al., "Purine metabolism and the microaerophily of Helicobacter pylori," A Microbiol, 168(6):448-458 (1997). 219. Mendz, et al., "The Entner-Doudoroff pathway in Helicobacter pylori," Arch Biochem Biophys, 312(2):349-356 (1994). 220. Mendz, GL and Hazell SL, "Ambioacid utilization by Helicobacter pylori," Int J Biochem Cell Biol. 27(10):1085-1093 (1995). 221. Mendz, GL and Hazell, SL, "Glucose phosphorylation in Helicobacter pylori," Arch Biochem Biophys, 300(1):522-525 (1993). 223. Mendz, GL, et al., "Pyruvate metabolism in Helicobacter pylori," Arch Microbiol, 162(3):187-192 (1994). 224. Mewes, et al., "MIPS: A database for genomes and protein sequences," Nucleic Acid Research, 30(1):31-34 (2002). Mitchell, "The GLN1 locus of Jaccharomyces cerevisiat encodes glutamine synthetase," Genetics, 111(2):243-258 (1985). 227. Moszer, "The Complete Genome of Bacillus Subtilis: From Sequence Annotation to Data Management and Analysis," FEBS Lett, 430(1-2):28-36 (1998). Moszer, et al., "Subtilist: the reference database for the bacillus subtilis genome," Nucleic Acids Res. 60(1):62-65 (2002). Mulquiney, PJ and Kuchel, PW, "Model of 2,3-bisphosphoglycerate metabolism in thuman erythros/te based on detailed enzyme kinetic equations: computer simulation and metabolic control analysis," Biochem J. 342(Pt 3):597-604 (1999). Murray, M and Greenberg, ML, "Expression of yeast INM1 encoding inosito monophosphatase is regulated by inositol, carbon source and growth stage and is decreased by lithium and valproate," Mol Microbiol, 36(3):651-661 (2000). Nedenskov, "Nutritional requirements for growth of Helicobacter pylori," Appl Entificio Apple All Pages and is decreased by lithium and valproate, "Mol Microbiol, 36(3)	212.	Biophys Acta, 1244(2-3):269-276 (1995).
214. Mendz, et al., "De novo synthesis of pyrimidine nucleotides by Helicobacter pylori," Appl Bacteriol, 77(1):1-8 (1994). 215. 216. 217. Mendz, et al., "In situ characterization of Helicobacter pylori arginase," Biochim Biophys Acta, 1388(2):465-477 (1998). 218. Mendz, et al., "Purine netabolism and the microaerophily of Helicobacter pylori," A Microbiol, 168(6):448-456 (1997). 219. Mendz, et al., "The Entner-Doudoroff pathway in Helicobacter pylori," Arch Biocher Biophys, 312(2):349-356 (1994). 220. Mendz, GL and Hazell SL, "Ambioacid utilization by Helicobacter pylori," Int J Biochem Cell Biol, 27(10):1085-1093 (1995). 221. 222. Mendz, GL and Hazell, SL, "Glucose phosphoralation in Helicobacter pylori," Arch Biochem Biophys, 300(1):522-525 (1993). 223. Mendz, GL, et al., "Pyruvate metabolism in Helicobacter pylori," Arch Microbiol, 162(3):187-192 (1994). 224. 225. Mewes, et al., "MIPS: A database for genomes and protein sequences," Nucleic Acid Research, 30(1):31-34 (2002). 226. Mitchell, "The GLN1 locus of Saccharomyces cerevisiae encodes glutamine synthetase," Genetics. 111(2):243-258 (1985). 227. Moszer, "The Complete Genome of Bacillus Subtilis: From Sequence Annotation to Data Management and Analysis," FEBS Lett, 430(1-2):28-36 (1998). 228. Moszer, et al., "Subtilist: the reference database for the bacillus subtilis genome," Nucleic Acids Res, 30(1):62-65 (2002). Mulquiney, PJ and Kuchel, PW, "Model of 2,3-bisphosphoglycerate netabolism in thuman erythrosyte based on detailed enzyme kinetic equations: computer simulation and metabolic control analysis," Biochem J, 342(Pt 3):597-604 (1999). Murray, M and Greenberg, ML, "Expression of yeast INM1 encoding inositel monophosphatase is regulated by inositol, carbon source and growth stage and is decreased by lithium and valproate," Mol Microbiol, 36(3):651-661 (2000). Nearnskov, "Nutritional requirements for growth of Helicobacter pylori," Appl Entylorobiol, 60(9):3450-3453 (1994). Nissen, et al., "Expression of a cytoplasmic transhydrogenase i	213.	
 215. 216. 217. Mendz, et al., "In stu characterization of Helicobacter pylori arginase," Biochim Biophys Acta, 1388(3):465-477 (1998). 218. Mendz, et al., "Purine metabolism and the microaerophily of Helicobacter pylori," A Microbiol, 168(6):448-458 (1997). 219. Mendz, et al., "The Entner-Doudoroff pathway in Helicobacter pylori," Arch Biochem Biophys, 312(2):349-356 (1994). 220. Mendz, GL and Hazell SL, "Amhoacid utilization by Fielicobacter pylori," Int J Biochem Cell Biol, 27(10):1085-1093 (1995). 221. 222. Mendz, GL and Hazell, SL, "Glucose phosphory lation in Helicobacter pylori," Arch Biochem Biophys, 300(1):522-525 (1993). 223. Mendz, GL, et al., "Pyruvate metabolism in Helicobacter pylori," Arch Microbiol, 162(3):187-192 (1994). 224. 225. Mewes, et al., "MIPS: A database for genomes and protein sequences," Nucleic Acid Research, 30(1):31-34 (2002). 226. Mitchell, "The GLN1 locus of Baccharomyces cerevisiae encodes glutamine synthetase," Genetics, 111(2):243-258 (1985). 227. Moszer, "The Complete Genome of Bacillus Subtilis: From sequence Annotation to Data Management and Malysis," FEBS Lett, 430(1-2):28-36 (1998). 228. Moszer, et al., "Subtilist: the reference database for the bacillus subtilis genome," Nucleic Acids Res. 80(1):62-65 (2002). 228. Mulquiney, P1 and Kuchel, PW, "Model of 2,3-bisphosphoglycerate netabolism in thuman erythroy te based on detailed enzyme kinetic equations: computer simulation and metabolic control analysis," Biochem J, 342(Pt 3):597-604 (1999). 230. Murray, M and Greenberg, ML, "Expression of yeast INM1 encoding inositel monophosphatase is regulated by inositol, carbon source and growth stage and is decreased by lithium and valproate," Mol Microbiol, 36(3):651-661 (2000). 231. Nedenskoy, "Nutritional requirements for growth of Helicobacter pylori," Appl Enviterobiol, 60(9):3450-3453 (1994). Nissen, et al., "Expressi	214.	Mendz, et al., "De novo synthesis of pyrimidine nucleotides by Helicobacter pylori," J
 216. 217. Mendz, et al., "In stu characterization of Helicobacter pylori arginase," Biochim Biophys Acta, 1388(3):465-477 (1998). 218. Mendz, et al., "Purine metabolism and the microaerophily of Helicobacter pylori," A Microbiol, 168(6):448-456 (1997). 219. Mendz, et al., "The Entner-Doudoroff pathway in Helicobacter pylori," Arch Biocher Biophys, 312(2):349-356 (1994). 220. Mendz, GL and Hazell SL, "Amhoacid utilization by Fielicobacter pylori," Int J Biochem Cell Biol, 27(10):1085-1093 (1995). 221. 222. Mendz, GL and Hazell, SL, "Glucose phosphor/lation in Helicobacter pylori," Arch Biochem Biophys, 300(1):522-525 (1993). 223. Mendz, GL, et al., "Pyruvate metabolism in Helicobacter pylori," Arch Microbiol, 162(3):187-192 (1994). 224. 225. Mewes, et al., "MIPS: A database for genomes and protein sequences," Nucleic Acid Research, 30(1):31-34 (2002). 226. Mitchell, "The GLN1 locus of Saccharomyces cerevisiae encodes glutamine synthetase," Genetics, 111(2):243-258 (1985). 227. Moszer, "The Complete Genome of Bacillus Subtilis: From Sequence Annotation to Data Management and Analysis," FEBS Lett, 430(1-2):28-36 (1998). 228. Moszer, et al., "Subtilist: the reference database for the bacillus subtilis genome," Nucleic Acids Res. 80(1):62-65 (2002). 229. Mulquiney, PJ and Kuchel, PW, "Model of 2,3-bisphosphoglycerate netabolism in thuman erythrosyte based on detailed enzyme kinetic equations: computer simulation and metabolic control analysis," Biochem J, 342(Pt 3):597-604 (1999). 230. Murray, M and Greenberg, ML, "Expression of yeast INM1 encoding inositol monophosphatase is regulated by inositol, carbon source and growth stage and is decreased by lithium and valproate," Mol Microbiol, 36(3):651-661 (2000). 231. Nedenskov, "Nutritional requirements for growth of Helicobacter pylori," Appl Ens. Microbiol, 60(9):33450-3453 (1994). Nissen, et al., "Expression of a cyt	215.	
 Mendz, et al., "In stu characterization of Helicobacter pylori arginase," Biochim Biophys Acta, 1388(2):465-477 (1998). Mendz, et al., "Purine rhetabolism and the microaerophily of Helicobacter pylori," A Microbiol, 168(6):448-45k (1997). Mendz, et al., "The Entner-Doudoroff pathway in Helicobacter pylori," Arch Biochem Biophys, 312(2):349-356 (1994). Mendz, GL and Hazell SL, "Amhaoacid utilization by Helicobacter pylori," Int J Biochem Cell Biol, 27(10):1085-1093 (1995). Mendz, GL and Hazell, SL, "Glucose phosphop lation in Helicobacter pylori," Arch Biochem Biophys, 300(1):522-525 (1993). Mendz, GL, et al., "Pyruvate metabolism in Helicobacter pylori," Arch Microbiol, 162(3):187-192 (1994). Mewes, et al., "MIPS: A database for genomes and protein sequences," Nucleic Acid Research, 30(1):31-34 (2002). Mitchell, "The GLN1 locus of Saccharomyces cerevisiat encodes glutamine synthetase," Genetics, 111(2):243-258 (1985). Moszer, "The Complete Genome of Bacillus Subtilis: From Sequence Annotation to Data Management and Analysis," FEBS Lett, 430(1-2):28-36 (1998). Moszer, et al., "Subtilist: the reference database for the bacillus subtilis genome," Nucleic Acids Res. 80(1):62-65 (2002). Mulquiney, PJ and Kuchel, PW, "Model of 2,3-bisphosphoglycerate netabolism in thuman erythrosyte based on detailed enzyme kinetic equations: computer simulation and metabolic control analysis," Biochem J, 342(Pt 3):597-604 (1999). Murray, Mand Greenberg, ML, "Expression of yeast INM1 encoding inosited monophosphatase is regulated by inositol, carbon source and growth stage and sedecreased by lithium and valproate," Mol Microbiol, 36(3):651-661 (2000). Nedenskov, "Nutritional requirements for growth of Helicobacter pylori," Appl Enkimicrobiol, 60(9):3450-3453 (1994). Nissen, et al., "Expression of a cytoplasmic transhydrogenase in Saccharomyces 		
218. Mendz, et al., "Purine metabolism and the microaerophily of Heficobacter pylori," A Microbiol, 168(6):448-458 (1997). 219. Mendz, et al., "The Entner-Doudoroff pathway in Helicobacter pylori," Arch Biocher Biophys, 312(2):349-356 (1994). 220. Mendz, GL and Hazell SL, "Amhaoacid utilization by felicobacter pylori," Int J Biochem Cell Biol, 27(10):1085-1093 (1995). 221. 222. Mendz, GL and Hazell, SL, "Glucose phosphor lation in Helicobacter pylori," Arch Biochem Biophys, 300(1):522-525 (1993). 223. Mendz, GL, et al., "Pyruvate metabolism is Helicobacter pylori," Arch Microbiol, 162(3):187-192 (1994). 224. 225. Mewes, et al., "MIPS: A database for genomes and protein sequences," Nucleic Acid Research, 30(1):31-34 (2002). 226. Mitchell, "The GLN1 locus of Saccharomyces cerevisiae encodes glutamine synthetase," Genetics, 111(2)/243-258 (1985). 227. Moszer, "The Complete Genome of Bacillus Subtilis: From Sequence Annotation to Data Management and Analysis," FEBS Lett, 430(1-2):28-36 (1998). 228. Moszer, et al., "Subtilist: the reference database for the bacillus subtilis genome," Nucleic Acids Res. 30(1):62-65 (2002). Mulquiney, PJ and Kuchel, PW, "Model of 2,3-bisphosphoglycerate netabolism in thuman erythrosyte based on detailed enzyme kinetic equations: computer simulation and metabolic control analysis," Biochem J, 342(Pt 3):597-604 (1999). Murray, M and Greenberg, ML, "Expression of yeast INM1 encoding inosited monophosphatase is regulated by inositol, carbon source and growth stage and secrepsed by lithium and valproate," Mol Microbiol, 36(3):651-661 (2000). Nedenskov, "Nutritional requirements for growth of Helicobacter pylori," Appl Enk Microbiol, 60(9):3450-3453 (1994). Nissen, et al., "Expression of a cytoplasmic transhydrogenase in Saccharomyces	217.	
Mendz, et al., "The Entner-Doudoroff pathway in Helicobacter pylori," Arch Biochem Biophys, 312(2):349-356 (1994).	218.	Mendz, et al., "Purine metabolism and the microaerophily of Horicobacter pylori," Arch Microbiol, 168(6):448-456 (1997).
220. Mendz, GL and Hazell SL, "Amisoacid utilization by flelicobacter pylori," Int J Biochem Cell Biol, 27(10):1085-1093 (1995). 221. 222. Mendz, GL and Hazell, SL, "Glucose prosphorolation in Helicobacter pylori," Arch Biochem Biophys, 300(1):522-525 (1993). 223. Mendz, GL, et al., "Pyruvate metabolism in Helicobacter pylori," Arch Microbiol, 162(3):187-192 (1994). 224. 225. Mewes, et al., "MIPS: A database for genomes and protein sequences," Nucleic Acid Research, 30(1):31-34 (2002). 226. Mitchell, "The GLN1 locus of Saccharomyces cerevisias encodes glutamine synthetase," Genetics, 111(2):243-258 (1985). 227. Moszer, "The Complete Genome of Bacillus Subtilis: From sequence Annotation to Data Management and Analysis," FEBS Lett, 430(1-2):28-36 (1998). 228. Moszer, et al., "Subtilist: the reference database for the bacillus subtilis genome," Nucleic Acids Res, 50(1):62-65 (2002). Mulquiney, PJ and Kuchel, PW, "Model of 2,3-bisphosphoglycerate netabolism in thuman erythrotyte based on detailed enzyme kinetic equations: computer simulation and metabolic control analysis," Biochem J, 342(Pt 3):597-604 (1999). Murray, M and Greenberg, ML, "Expression of yeast INM1 encoling inositel monophosphatase is regulated by inositol, carbon source and growth stage and is decreased by lithium and valproate," Mol Microbiol, 36(3):651-661 (2000). 231. Negenskov, "Nutritional requirements for growth of Helicobacter pylori," Appl Envi Microbiol, 60(9):3450-3453 (1994). Nissen, et al., "Expression of a cytoplasmic transhydrogenase in Saccharomyces	219.	
221. 222. Mendz, GL and Hazell, SL, "Glucose phosphorylation in Helicobacter pylori," Arch Biochem Biophys, 300(1):522-525 (1993). 223. Mendz, GL, et al., "Pyruvate metabolism is Helicobacter pylori," Arch Microbiol, 162(3):187-192 (1994). 224. 225. Mewes, et al., "MIPS: A database for genomes and protein sequences," Nucleic Acid Research, 30(1):31-34 (2002). 226. Mitchell, "The GLN1 locus of Saccharomyces cerevisiae encodes glutamine synthetase," Genetics, 111(2):243-258 (1985). 227. Moszer, "The Complete Genome of Bacillus Subtilis: From Sequence Annotation to Data Management and Analysis," FEBS Lett, 430(1-2):28-36 (1998). 228. Moszer, et al., "Subtilist: the reference database for the bacillus subtilis genome," Nucleic Acids Res., 30(1):62-65 (2002). Mulquiney, PJ and Kuchel, PW, "Model of 2,3-bisphosphoglycerate netabolism in the human erythrosyte based on detailed enzyme kinetic equations: computer simulation and metabolic control analysis," Biochem J, 342(Pt 3):597-604 (1999). Murray, M and Greenberg, ML, "Expression of yeast INM1 encoding inosited monophosphatase is regulated by inositol, carbon source and growth stage and is decreased by lithium and valproate," Mol Microbiol, 36(3):651-661 (2000). 231. Necenskov, "Nutritional requirements for growth of Helicobacter pylori," Appl Envincerobiol, 60(9):3450-3453 (1994). Nissen, et al., "Expression of a cytoplasmic transhydrogenase in Saccharomyces	220.	Mendz, GL and Hazell SL, "Ammoacid utilization by Helicobacter pylori," Int J
 Biochem Biophys, 300(1):522-525 (1993) Mendz, GL, et al., "Pyruvate metabolism in Melicobacter pylori," Arch Microbiol, 162(3):187-192 (1994). Mewes, et al., "MIPS: A database for genomes and protein sequences," Nucleic Acid Research, 30(1):31-34 (2002). Mitchell, "The GLN1 locus of Saccharomyces cerevisiate encodes glutamine synthetase," Genetics, 111(2):243-258 (1985). Moszer, "The Complete Genome of Bacillus Subtilis: From Sequence Annotation to Data Management and Analysis," FEBS Lett, 430(1-2):28-36 (1998). Moszer, et al., "Subtilist: the reference database for the bacillus subtilis genome," Nucleic Acids Res. 50(1):62-65 (2002). Mulquiney, PJ and Kuchel, PW, "Model of 2,3-bisphosphoglycerate netabolism in the human erythrosyte based on detailed enzyme kinetic equations: computer simulation and metabolic control analysis," Biochem J, 342(Pt 3):597-604 (1999). Murray, M and Greenberg, ML, "Expression of yeast INM1 encoding inosited monophosphatase is regulated by inositol, carbon source and growth stage and is decreased by lithium and valproate," Mol Microbiol, 36(3):651-661 (2000). Necenskov, "Nutritional requirements for growth of Helicobacter pylori," Appl Env. Microbiol, 60(9):3450-3453 (1994). Nissen, et al., "Expression of a cytoplasmic transhydrogenase in Saccharomyces 	221.	
 Mendz, GL, et al., "Pyruvate metabolism in Helicobacter pylori," Arch Microbiol, 162(3):187-192 (1994). Mewes, et al., "MIPS: A database for genomes and protein sequences," Nucleic Acid Research, 30(1):31-34 (2002). Mitchell, "The GLN1 locus of Saccharomyces cerevisian encodes glutamine synthetase," Genetics, 111(2):243-258 (1985). Moszer, "The Complete Genome of Bacillus Subtilis: From Sequence Annotation to Data Management and Analysis," FEBS Lett, 430(1-2):28-36 (1998). Moszer, et al., "Subtil/ist: the reference database for the bacillus subtilis genome," Nucleic Acids Res. 30(1):62-65 (2002). Mulquiney, PJ and Kuchel, PW, "Model of 2,3-bisphosphoglycerate netabolism in the human erythrosyte based on detailed enzyme kinetic equations: computer simulation and metabolic control analysis," Biochem J, 342(Pt 3):597-604 (1999). Murray, M and Greenberg, ML, "Expression of yeast INM1 encoding inosital monophosphatase is regulated by inositol, carbon source and growth stage and is decreased by lithium and valproate," Mol Microbiol, 36(3):651-661 (2000). Nedenskov, "Nutritional requirements for growth of Helicobacter pylori," Appl Envi Microbiol, 60(9):3450-3453 (1994). Nissen, et al., "Expression of a cytoplasmic transhydrogenase in Saccharomyces 	222.	
224. 225. Mewes, et al., "MIPS: A database for genomes and protein sequences," Nucleic Acid Research, 30(1):31-34 (2002). 226. Mitchell, "The GLN1 locus of Saccharomyces cerevisian encodes glutamine synthetase," Genetics, 111(2):243-258 (1985). 227. Moszer, "The Complete Genome of Bacillus Subtilis: From Sequence Annotation to Data Management and Analysis," FEBS Lett, 430(1-2):28-36 (1998). 228. Moszer, et al., "Subtilist: the reference database for the bacillus subtilis genome," Nucleic Acids Res., 50(1):62-65 (2002). Mulquiney, PJ and Kuchel, PW, "Model of 2,3-bisphosphoglycerate netabolism in the human erythrosyte based on detailed enzyme kinetic equations: computer simulation and metabolic control analysis," Biochem J, 342(Pt 3):597-604 (1999). Murray, M and Greenberg, ML, "Expression of yeast INM1 encoding inosited monophosphatase is regulated by inositol, carbon source and growth stage and is decreased by lithium and valproate," Mol Microbiol, 36(3):651-661 (2000). 231. Negenskov, "Nutritional requirements for growth of Helicobacter pylori," Appl Envi Microbiol, 60(9):3450-3453 (1994). Nissen, et al., "Expression of a cytoplasmic transhydrogenase in Saccharomyces	223.	Mendz, GL, et al., "Pyruvate metabolism in Helicobacter pylori," Arch Microbiol,
Research, 30(1):31-34 (2002). Mitchell, "The GLN1 locus of Saccharomyces cerevisial encodes glutamine synthetase," Genetics, 111(2):243-258 (1985). Moszer, "The Complete Genome of Bacillus Subtilis: From Sequence Annotation to Data Management and Analysis," FEBS Lett, 430(1-2):28-36 (1998). Moszer, et al., "Subtilist: the reference database for the bacillus subtilis genome," Nucleic Acids Res, 50(1):62-65 (2002). Mulquiney, PJ and Kuchel, PW, "Model of 2,3-bisphosphoglycerate netabolism in the human erythrocyte based on detailed enzyme kinetic equations: computer simulation and metabolic control analysis," Biochem J, 342(Pt 3):597-604 (1999). Murray, M and Greenberg, ML, "Expression of yeast INM1 encoding inosital monophosphatase is regulated by inositol, carbon source and growth stage and is decreased by lithium and valproate," Mol Microbiol, 36(3):651-661 (2000). Nedenskov, "Nutritional requirements for growth of Helicobacter pylori," Appl Enxi Microbiol, 60(9):3450-3453 (1994). Nissen, et al., "Expression of a cytoplasmic transhydrogenase in Saccharomyces	224.	
 synthetase," Genetics, 111(2)/243-258 (1985). Moszer, "The Complete Genome of Bacillus Subtilis: From Sequence Annotation to Data Management and Analysis," FEBS Lett, 430(1-2):28-36 (1998). Moszer, et al., "Subtilist: the reference database for the bacillus subtilis genome," Nucleic Acids Res. 20(1):62-65 (2002). Mulquiney, PJ and Kuchel, PW, "Model of 2,3-bisphosphoglycerate metabolism in the human erythrocyte based on detailed enzyme kinetic equations: computer simulation and metabolic control analysis," Biochem J, 342(Pt 3):597-604 (1999). Murray, M and Greenberg, ML, "Expression of yeast INM1 encoding inosited monophosphatase is regulated by inositol, carbon source and growth stage and is decreased by lithium and valproate," Mol Microbiol, 36(3):651-661 (2000). Nedenskov, "Nutritional requirements for growth of Helicobacter pylori," Appl Envi Microbiol, 60(9):3450-3453 (1994). Nissen, et al., "Expression of a cytoplasmic transhydrogenase in Saccharomyces 	225.	
 Moszer, "The Complete Genome of Bacillus Subtilis: From Sequence Annotation to Data Management and Analysis," FEBS Lett, 430(1-2):28-36 (1998). Moszer, et al., "Subtilist: the reference database for the bacillus ubtilis genome," Nucleic Acids Res. 50(1):62-65 (2002). Mulquiney, PJ and Kuchel, PW, "Model of 2,3-bisphosphoglycerate metabolism in the human erythrocyte based on detailed enzyme kinetic equations: computer simulation and metabolic control analysis," Biochem J, 342(Pt 3):597-604 (1999). Murray, Mand Greenberg, ML, "Expression of yeast INM1 encoding inosited monophosphatase is regulated by inositol, carbon source and growth stage and is decreased by lithium and valproate," Mol Microbiol, 36(3):651-661 (2000). Necenskov, "Nutritional requirements for growth of Helicobacter pylori," Appl Envi Microbiol, 60(9):3450-3453 (1994). Nissen, et al., "Expression of a cytoplasmic transhydrogenase in Saccharomyces 	226.	synthetase," Genetics, 111(2)/243-258 (1985).
228. Moszer, et al., "Subtil ist: the reference database for the bacillus subtilis genome," Nucleic Acids Res., 50(1):62-65 (2002). Mulquiney, PJ and Kuchel, PW, "Model of 2,3-bisphosphoglycerate metabolism in the human erythrocyte based on detailed enzyme kinetic equations: computer simulation and metabolic control analysis," Biochem J, 342(Pt 3):597-604 (1999). Murray, M and Greenberg, ML, "Expression of yeast INM1 encoding inosited monophosphatase is regulated by inositol, carbon source and growth stage and is decreased by lithium and valproate," Mol Microbiol, 36(3):651-661 (2000). 231. Nevenskov, "Nutritional requirements for growth of Helicobacter pylori," Appl Envi Microbiol, 60(9):3450-3453 (1994). Nissen, et al., "Expression of a cytoplasmic transhydrogenase in Saccharomyces	227.	Moszer, "The Complete Genome of Bacillus Subtilis: From Sequence Annotation to
Mulquiney, PJ and Kuchel, PW, "Model of 2,3-bisphosphoglycerate metabolism in the human erythrocyte based on detailed enzyme kinetic equations: computer simulation and metabolic control analysis," Biochem J, 342(Pt 3):597-604 (1999). Murray, M and Greenberg, ML, "Expression of yeast INM1 encoding inosited monophosphatase is regulated by inositol, carbon source and growth stage and is decreased by lithium and valproate," Mol Microbiol, 36(3):651-661 (2000). Necenskov, "Nutritional requirements for growth of Helicobacter pylori," Appl Envi Microbiol, 60(9):3450-3453 (1994). Nissen, et al., "Expression of a cytoplasmic transhydrogenase in Saccharomyces	228.	Moszer, et al., "Subtilest: the reference database for the bacillus subtilis genome,"
 230. monophosphatase is regulated by inositol, carbon source and growth stage and is decreased by lithium and valproate," Mol Microbiol, 36(3):651-661 (2000). 231. Nedenskov, "Nutritional requirements for growth of Helicobacter pylori," Appl Envi Microbiol, 60(9):3450-3453 (1994). Nissen, et al., "Expression of a cytoplasmic transhydrogenase in Saccharomyces 	229.	Mulquiney, PJ and Kuchel, PW, "Model of 2,3-bisphosphoglycerate metabolism in the human erythrocyte based on detailed enzyme kinetic equations: computer simulation and metabolic control analysis," Biochem J, 342(Pt 3):597-604 (1999).
Nissen, et al., "Expression of a cytoplasmic transhydrogenase in Saccharomyces	230.	monophosphatase is regulated by inositol, carbon source and growth stage and is decreased by lithium and valproate," Mol Microbiol, 36(3):651-661 (2000).
	231.	<u>Microbiol</u> , 60(9):3450-3453 (1994).
Yeast, 18(1):19-32 (2001).	23/2.	cerevisiae results in formation of 2-oxoglutarate due to depletion of the NADPH pool,"
	233.	Nissen, et al., "Flux distributions in anaerobic, glucose-limited continuous cultures of

234.	151(2):129-134 (2000).
235.	<u>Res.</u> 27(1).29-34 (1999).
236.	Ruxes in Escherichia coii, Biotech Prog. 16:278-286 (2000).
237.	Olsson, et al., "Separate and simultaneous enzymatic hydrolysis and fermentation of wheat hemicellulose with recombinant xylose utilizing Saccharomyces cerevisiae Appl Brochem Biotechnol, 129-132:117-129 (2006).
238.	Otto, et al. "A mathematical model for the influence of fructose 6-phosphate ATP, potassium, ammonium and magnesium on the phosphofructokinase from raterythrocytes," Eur J Biochem, 49(1):169-178 (1974).
239.	Ouzquis CA and Karn DD "Global Proportion of the Matchalia Man of Escherichia
240.	Overbeek, et al., "WN: Integrated System for High-Throughput Genome Sequence Analysis and Metabolic Reconstruction" Nucleic Acids Res, 28(1):123-125 (2000).
241.	by Saccharomyces cerevisiae mitochondria," J Bacteriol, 1\$2(10):2823-2830 (2000).
242.	175(17):5520-5528 (1993).
243.	FEBS Lett, 428(3):245-249 (1998).
244.	mitochondria," <u>Biochim Biophys Acta</u> , 1459(2-3):363-369 (2000).
245.	(1997).
246.	and sulfate," J Biol Chem, 21/(32):22184-22190 (1999).
247.	identification and metabolic significance," J Bioenerg Biomerabr, 32(1):67-77 (2000).
248.	(2000).
249.	influenzae shows significant network redundancy," <u>J Theor Biol</u> , 215(1):67-82 (2002).
250.	Parks, "Metabolism of sterols in yeast," <u>CRC Crit Rev Microbiol</u> , 6(4):301-341 (1978).
251.	Parks, et al, "Use of sterol mutants as probes for sterol functions in the yeas Saccharonyces cerevisiae," Crit Rev Biochem Mol Biol, 34(6):399-404 (1999).
252.	
253.	Paulen, et al., "Unified inventory of established and putative transporters encoded within the complete genome of Saccharomyces cerevisiae," <u>FEBS Lett</u> , 430(1-2):110 25 (1998).
25/	Pearson, et al., "Comparison of DNA Sequences With Protein Sequences," Genomics, 46(1):24-36 (1997).
255.	Persson, et al., "Phosphate permeases of Saccharomyces cerevisiae: structure, function and regulation," <u>Biochim Biophys Acta</u> , 1422(3):255-272 (1999).

256.	Peterson, et al., "The Comprehensive Microbial Resource," <u>Nucleic Acids Res</u> , 29(1):123-125 (2001).
257.	Pharkya, et al., "Exploring the overproduction of amino acids using the bilevel optimization framework OptKnock," <u>Biotechnol Bioeng</u> , 84(7):887-899 (2003).
258.	Phelps, et al., "Metabolomics and microarrays for improved understanding of henotypic characteristics controlled by both genomics and environmental constraints." <u>Curr Opin Biotechnol</u> , 13(1):20-24 (2002).
259.	Pitson, et al., "The tricarboxylic acid cycle of Helicobacter pylori," <u>Eur J Biochem</u> , 260(1) \$258-267 (1999).
260.	Price, et al., "Determination of redundancy and systems properties of the methoolic network of Helicobacter pylori using genome-scale extreme pathway analysis," Genome Res, 12(5):760-769 (2002).
261.	Price, et al., "Genome-scale models of microbial cells: evaluating the consequences of constraints," Nat Nev Microbiol, 2(11):886-897 (2004).
262.	Price, et al., "Network-based analysis of metabolic regulation in the human red blood cell," <u>J Theor Biol</u> , 223(2):185-194 (2003).
263.	Przybyla-Zawisłak, et al., "Genes of succinyl-CoA ligase from Saccharomyces cerevisiae.," Eur J Biochem 258(2):736-743 (1998).
264.	Qian, et al., "Ethanol production from dilute-Acid softwood hydrolysate by co-culture," Appl Biochem Biotechnol, 134(\$):273-284 (2006).
265.	Reed, et al., "An expanded genome scale model of Discherichia coli K-12 (iJR904 GSM/GPR)," Genome Biol, 4(9):R5 (2003).
266.	Reed, JL and Palsson, BO, "Thirteen years of building constraint-based in silico models of Escherichia coli" J Bacteriol, 185(9):2692,2699 (2003).
267.	Regenberg, et al., "Substrate specificity and gene expression of the amino-acid permeases in Saccharomyces cerevisiae," <u>Cura Genet</u> , 36(6):317-328 (1999).
268.	Remize, et al., "Engineering of the pyravate dehydrogenase bypass in Saccharomyces cerevisiae: role of the cytosolic Mg(2+) and mitocrondrial K(+) acetaldehyde dehydrogenases Ald6p and Ald4p in acetate formation during alcoholic fermentation," Appl Environ Microbiol, 66(8): 151-3159 (2000).
269.	Ren, et al., "Genome-wide location and function of DNA binding proteins," Science, 290(5500):2306-2309 (2006).
270.	Repetto, B and Tzagoloff, A, "In vivo assembly of yeast mitochondrial alphaketoglutarate dehydrogenase complex," Mol Cell Biol, 11(8):3931-3939 (1991).
271.	Reynolds, DJ and Ponn, CW, "Characteristics of Helicobacter pylori growth in a defined medium and determination of its amino acid requirements," Microbiology, 140(Pt 10):2649 2656 (1994).
272.	Rhee, et al., "Activation of gene expression by a ligand-induced conformational change of a protein DNA complex," <u>J Biol Chem</u> , 273(18):11257-11266 (1998).
273.	Romero, PR and Karp, P, "Nutrient-Related Analysis of Pathway/Genome Databases," Pac Symp Biocomput, 471-482 (2001).
274.	Saie, MH, "Genome sequencing and informatics: new tools for biochemical discoveries," <u>Plant Physiol</u> , 117(4):1129-1133 (1998).
275.	Salgado, et al., Nucleic Acids Res, 29(1):72-74 (2001).
27/8.	Salmon, et al., "Global gene expression profiling in Escherichia coli K12. The effects of oxygen availability and FNR," J Biol Chem, 278(32):29837-29855 (2003).
277.	Sauer, et al., "Metabolic flux ratio analysis of genetic and environmental modulations of Escherichia coli central carbon metabolism," <u>J Bacteriol</u> , 181(21):6679-6688 (1999).

278.	Sauer, U and Bailey, JE, "Estimation of P-to-O Ratio in <i>Bacillus subtilis</i> and Its Influence on Maximum Riboflavin Yield," <u>Biotechnol Bioeng</u> , 64(6):750-754 (1999).
279.	Sauer, Uwe, "Evolutionary Engineering of Industrially Important Microbial Phenotypes," Adv in Biochem Eng Biotechnol, 73:129-169 (2001).
280.	Savageau, "Biochemical systems analysis. I. Some mathematical properties of the rate law for the component enzymatic reactions," <u>J Theor Biol</u> , 25(3):365-369 (1969).
281.	Schaaff-Gerstenschlager, I and Zimmermann, FK, "Pentose-phosphate pathway in Saccharomyces cerevisiae: analysis of deletion mutants for transketolase, transald ase, and gluose 6-phosphate dehydrogenase," <u>Curr Genet</u> , 24(5):373-376 (1993).
282.	Schaff, et al., "the Virtual cell" <u>Proceedings of the Pacific Symposium on Biocomputing</u> , 4:228-239 (1999).
283.	
284.	Schilling, "On Systems Biology and the Pathway Analysis of Metabolic Networks," Department of Biologineering, University of California, San Diego: La Jolla, p. 198-241 (2000).
285.	Schilling, CH and Palsson, BO, "Assessment of the Metabolic Capabilities of <i>Haemophilus influenzae</i> Ad Through a Genome-scale Pathway Analysis," <u>J Theor Biol</u> , 203(3):249-283 (2000).
286.	Schilling, CH and Palsson, BO, "The Underlying Pathway Structure of Biochemical Reaction Networks," Proc Natl Acad Sci U.S.A., 95(8) 4193-4198 (1998).
287.	Schilling, et al., "Combining Pathway Analysis with Flux Balance Analysis for the Comprehensive Study of Metabolic Systems," <u>Biotechnol Bioeng</u> , 71(4):286-306 (2000-2001).
288.	Schilling, et al., "Genome-scale metabolic model of Helicobacter pylori 26695," J Bacteriol, 184(16):4582-4593 (2002).
289.	Schilling, et al., "Metabolic Pathway Analysis, Basic Concepts and Scientific Applications in the Post-genomic Era," Biotechol Prog, 15(3):296-303 (1999).
290.	Schilling, et al., "Theory for the Systematic Definition of Metabolic Pathways and Their Use in Interpreting Metabolic Function from a Pathway-Oriented Perspective," J Theor Biol, 203(3):229-248 (2000).
291.	Schneider, et al., "The Escherichia coli gabDTPC operon specific gamma-aminobutyrate catabolism and nonspecific induction," <u>J Basteriol</u> , 184(24):6976-6986 (2002).
292.	Schuster, et al., "A general definition of metabolic pathways useful for systematic organization and analysis of complex metabolic networks," <u>Nature Biotechnol</u> , 18(3):326-332 (2000).
293.	Schuster, et al., Detection of elementary flux modes in biochemical networks: a promising too for pathway analysis and metabolic engineering," Trends Biotechnol, 17(2):53-60 (1999).
294.	Schuster et al., "Exploring the pathway structure of metabolism: decomposition into subnetworks and application to Mycoplasma pneumoniae," <u>Bioinformatics</u> , 18(2):351-361 (2002).
295.	Schuster, S and Hilgetag, C, "On elementary flux modes in biochemical reaction ystems at steady state," J Biol Syst, 2(2):165-182 (1994).
298.	Schwikowski, et al., "A network of protein-protein interactions in yeast," Nature Biotechnol, 18(12):1257-1261 (2000).
/ 297.	
298.	

	Selkov, et al., "Functional Analysis of Gapped Microbial Genomes: Amino Acid
299.	Metabolism of Thiobacillus Ferroxidans," Proc Natl Acad Sci U.S.A., 97(7):3509-3514
No.	(2000).
	Selkov, et al., "MPW: the metabolic pathways database," Nucleic Acids Res, 26(1):43-
300	45 (1998)
301.	Selkov, et al., "The metabolic pathway collection from EMP: the enzymes and
	metabolic pathways database," Nucleic Acids Res, 24(1):26-28 (1996).
	Sher Orr, et al., "Network motifs in the transcriptional regulation network of
302.	Escherichia coli," Nat Genet, 31(1):64-68 (2002).
303.	255151, 1115 5515, 5 1 (1) 15 15 15 15 15 15 15 15 15 15 15 15 15
304.	
304.	Silve, et al., "The immunosuppressant SR 31747 blocks cell proliferation by inhibiting
ا ممد ا	
305.	a steroid isomerase in Saccharomyces cerevisiae,' Mol Cell Biol, 16(6):2719-2727
	(1996).
	Skouloubris, et al., "The Helicobacter pylori Urel protein is not involved in urease
306.	activity but is essential for bacterial survival in vivo," <u>Infect Immun</u> , 66(9):4517-4521
	(1998).
307.	Smith, et al., "Functional analysis of the genes of yeast chromosome V by genetic
	footprinting.," <u>Science</u> , 274(3895):2069-2074 (1996).
308.	
309.	
	Sorlie, et al., "Gene expression patterns of breast carcinomas distinguish tumor
310.	subclasses with clinical implications," <u>Proc Nat Acad Sci U.S.A.</u> , 98(19):10869-10874
	(2001).
244	Stark, et al., "Amino acid utilisation and deamination of glutamine and asparagine by
311.	Helicobacter pylori," J Med Microbiol, 46(9). 793-800 (1997).
312.	Stephanopoulos, "Metabolic engineering," Curr Opin Biotechnol, 5(2):196-200 (1994).
	Summers, et al., "Saccharomyces cerevisiae cho2 quants are deficient in phospholipid
313.	methylation and cross-pathway regulation of inosito synthesis" Genetics, 120(4):909-
	922 (1988).
	Swartz, "A PURE approach to constructive biology.," Nat Biotechnol, 19(8):732-733
314.	(2001).
	Syvanen, "Accessing genetic variation: Genotyping single nucleotide polymorphisms.,"
315.	Nat Rev Genet, 2(12):330-942 (2001).
	Szambelan, et al., "Dse of Zymomonas mobilis and Saccharomyces cerevisiae mixed
316.	with Kluyveromyces fragilis for improved ethanol production from Jerusalem artichoke
3 10.	tubers,"Biotechnol Lett, 26(10):845-848 (2004).
247	Tamayo, et al., "Interpreting patterns of gene expression with self-organizing maps: methods and application to hematopoietic differentiation," Proc Natl Acad Sci U.S.A,.
317.	
240	96(6):29,07-2912 (1999).
318.	
319.	Tanguchi, M and Tanaka, T, "Clarification of interactions among microorganisms and
	development of co-culture system for production of useful substances," Adv Biochets
<u></u>	Eng Biotechnol, 90:35-62 (2004).
3/20.	Tao, et al., "Engineering a homo-ethanol pathway in Escherichia coli: increased
	glycolytic flux and levels of expression of glycolytic genes during xylose
	fermentation," <u>J Bacteriol</u> , 183(10):2979-2988 (2001).

321.	(1999).
328	Thomas, "Boolean Formalization of Genetic Control Circuits," <u>J Theor Biol</u> , 42(3):563-585 (1973).
323.	Thomas, "Logical Analyses of Systems Comprising Feedback Loops," J Theor Biol, 73(4):631-656 (1978).
324.	Thomas, D and Surdin-Kerjan, Y, "Metabolism of sulfur amino acids in Saccharomyces cerevisiae," Microbiol Mol Biol Rev, 61(4):503-532 (1997).
325.	Tomb, et al., "The complete genome sequence of the gastric pathogen Helicopacter pylori," Naure, 388(6642):539-547 (1997).
326.	Trotter, et al., "A genetic screen for aminophospholipid transport mutants identifies the phosphatidylinositol 4-kinase, STT4p, as an essential component in phosphatidylserine metabolism," J Biol Chem, 273(21):13189-13196 (1998).
327.	Uetz, et al., "A comprehensive analysis of protein-protein interactions in Saccharomyces cerevisiae," Nature, 403(6770):623-627 (2000).
328.	Van den Berg, MA and Steensma, HY, "ACS2, a Saccharomyces cerevisiae gene encoding acetyl-coenzyme A synthetase, essential for growth on glucose," <u>Eur J Biochem</u> , 231(3):704-713 (1995).
329.	van Dijken, et al., "Alcoholic fermentation by 'non-fermentative' yeasts," Yeast, 2(2):123-127 (1986).
330.	van Dijken, et al., "Kinetics of growth and sugar consumption in yeasts," Antonie Van Leeuwenhoek, 63(3-4):343-352 (1993).
331.	Vanrolleghem, et al., "Validation of a Metabolic Network for Saccharomyces cerevisiae Using Mixed Substrate Studies," Biotechnol Prog, 12(4):434-448 (1996).
332.	Varma, A and Palsson, BO, "Metabolic capabilities of <i>Escherichia coli</i> . II: Optimal Growth Patterns.," J Theor Biol, 165:203-522 (1993).
333.	Varma, A and Palsson, BO, "Metabolic capabilities of <i>Escherichia coli</i> : I. Synthesis of Biosynthetic Precursors and Cofactors," J Theor Biol., 165:477-502 (1993).
334.	Varma, A and Palsson, BO, "Parametric sensitivity of stoichiometric flux balance models applied to wild-type Escherichia coli metabolish," <u>Biotechnol Bioeng</u> , 45(1):69-79 (1995).
335.	Varma, A and Palsson, FO, "Predictions for Oxygen Supply Control to Enhance Population Stability of Engineered Production Strains," <u>Biotechnol Bioeng</u> , 43(4):275-285 (1994).
336.	Environ Microbiol, 60(10):3724-3731 (1994).
337.	Bioeng, 42(1):39-73 (1993).
338.	Unger Various Oxygenation Rates., Appl Environ Microbiol, 39(8):2403-2473 (1993).
339.	Vopin Biotechnol, 10(2):146-150 (1999).
3/0.	Velculescu, et al., "Analysing uncharted transcriptomes with SAGE," <u>Trends Genet</u> , 16(10):423-425 (2000).
341	

	•
342.	Verduyn, "Physiology of yeasts in relation to biomass yields," <u>Antonie Van Leeuwenhoek</u> , 60(3-4):325-353 (1991).
343.	Verduyn, et al., "A theoretical evaluation of growth yields of yeasts," Antonie Van Leeuwenhoek, 59(1):49-63 (1991).
344.	Verduyn, et al., "Energetics of Saccharomyces cerevisiae in anaerobic glucose-limited hemostat cultures," J Gen Microbiol, 136:405-412 (1990).
345.	Vissing, et al., "Paradoxically Enhanced Glucose Production During Exercise in Humans with Blocked Glycolysis Caused by Muscle Phosphofructokinase Deficiency," Neurology, 47(3):766-771 (1996).
346.	Wang, et al., "Computer-aided baker's yeast fermentations," <u>Biotechnol and Pioeng</u> , 19(1):69-86 (1977).
347.	Wang, et al., "Computer Control of Bakers' Yeast Production," <u>Biotechnol and Bioeng</u> , 21:975-995 (1979).
348.	
349.	Wen, et al., "Large-scale temporal gene expression mapping of central nervous system development," Proc Natl Acad Sci U.S.A., 95(1):334-339 (1998).
350.	Wiback, SJ and Palsson, BO, "Extreme pathway analysis of human red blood cell metabolism," Biophys J, 83 808-818 (2002).
351.	Wieczorke, et al., "Concurrent knock-out of at least 20 transporter genes is required to block uptake of hexoses in Saccharomyces cerevisiae." FEBS Lett, 464(3):123-128 (1999).
352.	
353.	Wingender, et al., "The TRANSFAC system on gene expression regulation," <u>Nucleic Acids Res</u> , 29(1):281-283 (2001).
354.	X
355.	Wong, P., et al., "Mathematical Model of the Lac Operon: Inducer Exclusion, Catabolite Repression, and Diauxic Growth on Glucose and Lactose," <u>Biotechnol Prog</u> , 13(2):132-143 (1997).
356.	Yamada, et al., "Effects of common polymorphisms on the properties of recombinant human methylenetetrahydrofolate reductase," Proc Natl Acad Sci U.S.A., 98(26):14853-14858 (2001).
357,	Yeung, et al., "Reverse engineering gene networks using singular value decomposition and robust regression," <u>Proc Natl Acad Sci U.S.A.</u> , 99(9):6163-6168 (2002).
358.	Yeung, et al., <u>Bioinformatics</u> , "Model-based clustering and data transformations for gene expression data," 17(10):977-87 (2001).
359.	Res, 29(3):688-692 (2001).
360.	Zanella, A and Bianchi, P, "Red cell pyruvate kinase deficiency: from genetics to clinical planifestations," <u>Bailliere's Best Pract Res Clin Haematol</u> 13(1):57-81 (2000)
361.	
362.	Zhu, J and Zhang, MO, "SCPD: a promoter database of the yeast Saccharomyces corevisiae," Bioinformatics, 15(7-8):607-611 (1999).
363.	
364.	Zweytick, et al., "Biochemical characterization and subcellular localization of the sterol C-24(28) reductase, erg4p, from the yeast saccharomyces cerevisiae," <u>FEBS Lett.</u> , 470(1):83-87 (2000).
365.	110(1).05 01 (2000).

EXHIBIT A U.S. Application No. 09/923,870 09923870 - GAU: 1631

366.	
367.	
368.	RL ca.expasy.org/sprot/, protein database SWISS—PROT.
369.	
370.	URL dchip org, dChip software.
371.	URL Dictionary com pgs 1-2 (2004), Matrix.
372.	
373.	
374.	
375.	URL genome.ad.jp/kegg/, Kyoto Encyclopedia of Genes and Genomes database (KEGG).
376.	URL Genome.jp Website, KEGG Bacillus subtillis, 1-7 (2005).
377.	
378.	
379.	
380.	
381.	
382.	URL ncbi.nlm.nih.gov/entrez/query.fcgi?db=Genome, The NCBI Entrez Genome database

all references duplicates of 6/18/09 IDS

/Russell S. Negin/

09/22/2009